# SUBJECT INDEX

Actinomyces spp.

A	fatty acid antibiotics and,	Aeropyrum pernix
Aa-Pri2 gene	306	horizontal gene transfer in
hydrophobins and, 626-27	Actinomycetes	prokaryotes and, 716,
ABH genes	novel thiols and, 333, 347	720, 728
hydrophobins and, 626–27,	symbiosis and	Agaricus bisporus
631, 638–39	fungus-growing ants,	hydrophobins and, 626-27,
A-B type toxins	357–75	631, 635, 638–39
anthrax and, 647	Actinoplanes philippinensis	aglU gene
acc genes	novel thiols and, 347	bacterial gliding motility
fatty acid antibiotics and,	Adaptation	and, 57
308–9, 311	fungal pathogenesis and,	AgrC/AgrA virulence system
AcCys-GlcNα(1->1)Ins	743, 754–55	quorum sensing and,
novel thiols and, 333,	horizontal gene transfer in	181–82
345	prokaryotes and, 709	Agrobacterium tumefaciens
Acetyl-CoA carboxylase	Adaptive clones	quorum sensing and, 167,
fatty acid antibiotics and,	recombination and	171–74, 176–77
310–11	bacterial population	Agrocybe aegerita
Achromatium oxaliferum	structure, 561, 563–65, 570	hydrophobins and, 626–27
ammonia-oxidizing bacteria and, 516	*	ahpC gene
big bacteria and, 116–19	Adaptive immune response immune checkpoints in	fatty acid antibiotics and, 320
•	viral latency and, 532,	thiol-redox pathways and,
acp genes anthrax and, 650	540–41	38–39
fatty acid antibiotics and,	Adenylate cyclase	AI-2 synthases
308–9, 316	anthrax and, 647	quorum sensing and,
Acquired immunity	Advective flow	185–86
immune checkpoints in	big bacteria and, 105	ainS gene
viral latency and, 531–32	Adventurous gliding	quorum sensing and,
acrAB-encoded multidrug	bacterial gliding motility	185
efflux pump	and, 49, 54, 57–58	Air-exposed fungal surfaces
fatty acid antibiotics and,	Aerial growth	coating
319	hydrophobins and, 625,	hydrophobins and,
Acromyrmex spp.	630–31, 634	634–35
symbiosis and	Aerobacter aerogenes	Alcaligenes eutrophus
fungus-growing ants, 359,	coliform group	periplasmic stress and
362, 364, 367, 372, 374	bacteriology and, 204	extracytoplasmic function
Actinobacillus	Aeromonas spp.	sigma factors, 596
actinomycetecomitans	coliform group	alg genes
fatty acid antibiotics and,	bacteriology and, 210,	bacterial gliding motility
322	212	and, 53

quorum sensing and, 174

periplasmic stress and

extracytoplasmic function terrestrial environments. 499-502 sigma factors, 601-3 Allomyces arbuscula DNA chip technology, history of research, 6-7 511-12 ALS gene family Escherichia coli, 516 fungal pathogenesis and, economic importance, 489-90 Alternative energy sources functional genomics, nonreplicating latency of 511-12 Mycobacterium future advances in tuberculosis and, 139. molecular techniques. 149-51 509-13 Aminoacyl-tRNA synthetases future perspectives, 511-16 horizontal gene transfer in x-subclass, 513 prokarvotes and, 709, genome sequencing. 729, 732-33, 735 511-12 Ammonia-oxidizing bacteria global nitrogen cycle, amoA and other 488-89 heterotrophic nitrifiers, protein-encoding genes, 510-11 513-14 Annamox bacteria, 514 improvements of existing applications, 514-15 technologies, 509-10 bioremediation of indicator organisms, 515-16 pollutants, 515 introduction, 486-92 biotechnology, 514-15 chemolitho-autotrophic isolation of ammonia oxidation. ammonia-oxidizing 486-87 bacteria from conclusions, 516 environment, 491-92 diversity and distribution limitations, 512 based on 16S rDNA linking identification with analyses activity, 511 aquatic environments, miscellaneous nitrifiers. 502-3 513-14 biofilms, 497-99 modeling, 514-15 biofilters, 497-99 necessity to combine methods, 512 bioreactors, 497-99 characterization. nitrification-associated 497-505 problems, 490-91 marine environments. nitrite-oxidizing bacteria, 503-4 phylogenetically-based non-16S PCR techniques primers and probes, for strain identification

amoA gene as marker.

amo-like sequences,

505-6

506-7

493-97

phylogeny of culture

collection, 492-93

sewage, 497-99

miscellaneous markers within rRNA operon, 507 primer and probe development, 509-10 tracking populations enrichments vs direct extraction results. 508-9 laboratory experiments, quantitative techniques targeting amoA and 16S rDNA, 507-8 utilization, 489-90 Ammonium bicarbonate biological weapons and, 244 amoA gene ammonia-oxidizing bacteria and, 505-8. 510-13 Amphipathic film hydrophobins and, 625 Amphotericin B fungal pathogenesis and, 752 Ampicillin bacteriophage therapy and, 447 Amplified fragment length polymorphisms (AFLPs) anthrax and, 663 Amplified ribosomal DNA restriction analysis (ARDRA) ammonia-oxidizing bacteria and, 502 Amycolatopsis methanolica novel thiols and, 344 Anabaena variabilis bacterial gliding motility and, 61 Anacystis nidulans thiol-redox pathways and, Ancestral DNA

recombination and bacterial population structure, 567

Anergy

toxic shock syndrome and, 93

Annamox bacteria ammonia-oxidizing bacteria and, 494, 514

Anomalous nucleotide composition horizontal gene transfer in prokaryotes and, 717

Anoxia

big bacteria and, 113, 127–29

Anthrax

Bacillus anthracis and, 647–63

Antibacterial agents bacteriophage therapy and, 437-48

fatty acid antibiotics and, 305-25

Antibiotics

bacteriophage therapy and, 437, 440–41, 445–47 dairy bacteria phages and, 290

fatty acids and, 305-25 fungal pathogenesis and, 752

nonreplicating latency of *Mycobacterium* tuberculosis and, 144 novel thiols and, 345, 348 quorum sensing and, 165, 170, 172–73

bacterial population structure, 577, 584 symbiosis and fungus, growing ants 35

recombination and

fungus-growing ants, 357, 364–66, 371–74

toxic shock syndrome and, 84, 86, 90

Antibodies

antigenic variation at red cell surface in malaria and, 679–80, 683, 685, 696

bacteriophage therapy and, 444

fungal pathogenesis and, 760

Antigenic variation infected red cell surface in malaria and, 673–97

Antioxidants novel thiols and, 333, 343, 348

"Antisenescent" red cell antibody

antigenic variation at red cell surface in malaria and, 696

Ants

fungus-growing symbiosis and, 357–75 Apical membrane polarized epithelium and

pathogens, 407, 409, 413–17, 425

Apoptosis

immune checkpoints in viral latency and, 539-40 toxic shock syndrome and, 93 viruses and interferons,

269, 274

horizontal gene transfer in prokaryotes and, 730 aprA gene

quorum sensing and, 169

Apterostigma spp. symbiosis and fungus-growing ants, 359, 361, 370, 372-73

Aquatic environments ammonia-oxidizing bacteria and, 502–3 hydrophobins and, 630–34 Aquifex spp. fatty acid antibiotics and, 309 horizontal gene transfer in

prokaryotes and, 711, 716, 719–21, 723, 726–28

Archaea

ammonia-oxidizing bacteria and, 494, 516 big bacteria and, 115 horizontal gene transfer in prokaryotes and, 709–36

Archaebacteria aerobic phototrophic novel thiols and, 333, 337, 348

Archaeoglobus fulgidus horizontal gene transfer in prokaryotes and, 716, 720, 726–28

Arsenophonus spp. coliform group bacteriology and, 206, 209

Ascobolus immersus homology-dependent gene silencing in fungi and, 382, 384–86, 389

asg genes

quorum sensing and, 187 Aspergillus fumigatus biological weapons and, 238

fungal pathogenesis and, 744, 748, 751, 753–54, 758–62

hydrophobins and, 626–27, 634

Aspergillus spp.

fungal pathogenesis and, 744, 746, 751 hydrophobins and, 626–27, 634

Assortative recombination recombination and bacterial population structure, 565–66 ATP/ADP translocases

"Background" population horizontal gene transfer in toxins, 654 prokaryotes and, 709, 736 cellular model of action. recombination and 656 bacterial population Atta spp. edema factor, 657 structure, 572-73 symbiosis and functional organization, Bacterial gliding motility fungus-growing ants, 359, adventurous gliding, 57-58 362, 365-67, 369-70 655-57 att genes lethal factor, 657 cell division, 66 mode of action, 655-57 cell-surface dairy bacteria phages and, 291-92 pathogenesis, 657-58 polysaccharides, 66 regulatory pathways conclusions, 68-69 toxic shock syndrome and, 88-90 major virulence factor control of cell movement. 58-59 Attine ants regulation of synthesis, symbiosis and 658-59 cyanobacteria, 60-62 fungus-growing ants, 359, miscellaneous regulated Cytophaga-Flavobacterium 362-75 components, 660 group, 62-66  $\sigma^{\rm B}$  factor, 660 filamentous cyanobacteria. Autoinducers S-layer regulation. 60-62 quorum sensing and, 165-89 659-60 Flavobacterium vaccines, 661 johnsoniae, 64-66 Avian typhosis bacteriophage therapy and, virulence plasmids, 650-51 introduction, 50-52 439 Bacillus cereus group motile-nonspreading Azoles Bacillus anthracis and. mutants, 66 fungal pathogenesis and, 647-63 multiple systems for cell 752 Bacillus spp. movement, 54, 56-59 Mycoplasma spp., 67-68 horizontal gene transfer in R prokaryotes and, 716, myxobacteria, 54 720-21, 726-28 Babesia bovis polysaccharides, 60-62 antigenic variation at red novel thiols and, 347-48 prospects, 68-69 cell surface in malaria Bacillus subtilis social gliding, 55-57 and, 695 Synechocystis PCC6803, anthrax and, 659-60 Bacillus anthracis dairy bacteria phages and. biological weapons and. 288, 294, 296 twitching motility, 52-54, 236-39, 247-48 fatty acid antibiotics and, 56-59 conclusions, 663 308-9, 323-24 type IV pili, 52-54, 60-62 detection, 662 Bacterial mats horizontal gene transfer in big bacteria and, 105-6, disease, 649 prokaryotes and, 716, early steps of infection, 649 719-22, 726-28 116-17, 119-31 periplasmic stress and ecology, 662 Bacteriology introduction, 648 extracytoplasmic function coliform group and, life cycle, 648 sigma factors, 596, 201-24 organism, 649-51 602-4, 614 history of research, 12 phylogeny, 662 quorum sensing and, Bacteriophage therapy prophylaxis, 661-63 179-82, 186, 188 aims, 437-38 surface structures thiol-redox pathways and, background, 437-38 capsule, 651-52 25, 34 early trials, 438-41 exosporium, 651 Bacillus thuringiensis immunogenicity, 444-45 S-layer, 652-54 anthrax and, 662 polyvalency, 441-44

problems, 441-45 overview, 115-19 questions, 441-45 scale of living organisms, recent results, 445-48 resistance, 445 sediment-water interface, restriction/modification, 444 112-15 Bacteroides spp. size limit of prokaryotes, coliform group 107-11 bacteriology and, 211-12 summary, 131-32 Basolateral membrane Binary fission polarized epithelium and 296 recombination and pathogens, 407-13, 419, bacterial population birA gene 421-25 structure, 561 "Bastions of polymorphism" Biochemistry recombination and bacterial gliding motility bacterial population and, 49 structure, 567 nonreplicating latency of B-domain Mycobacterium anthrax and, 647 tuberculosis and, 145-46 Beauveria bassiana toxic shock syndrome and, hydrophobins and, 636 77 Biofertilizers Beggiatoa sp. big bacteria and, 106, ammonia-oxidizing 115-17, 119-31 bacteria and, 504 Beta-propiolactone Biofilms biological weapons and, ammonia-oxidizing 244 bacteria and, 497-99 Bifidobacterium spp. quorum sensing and, 165, coliform group 170 - 71Bovine hemorrhagic bacteriology and, 211-12 **Biofilters** Big bacteria ammonia-oxidizing anoxia, 127-29 bacteria and, 497-99 chemotaxis, 111-13 Biological weapons diffusion, 107-11 decontamination, 243-45 diffusive boundary layer, history, 237-40 124-27 incident response, 245-49 Brassica napus ecological niches, 119-30 introduction, 236-37 electron acceptor, 130-31 levels of protection. 318 - 19fast swimmers, 123-24 246-47 flowing water, 119-21 personal protection, monopolizing substrates, 241-43 111 - 12128, 130 properties, 240-43 Brucella suis nitrate, 127-29 Bioluminescence one-dimensional opposed quorum sensing and, 238 diffusion gradients, 167-68 Buchnera sp. 121 - 23**Biomass** big bacteria and, 105-32 organized communities, 123-24 Bioreactors

ammonia-oxidizing bacteria and, 497-99 Bioremediation ammonia-oxidizing bacteria and, 515 Biotechnology ammonia-oxidizing bacteria and, 514-15 dairy bacteria phages and, fatty acid antibiotics and,

Blastomyces dermatitidis fungal pathogenesis and, 746, 748, 751 Bordetella pertussis anthrax and, 657

Borrelia burgdorferi horizontal gene transfer in prokarvotes and, 716. 719, 723, 726-28 quorum sensing and, 186

Borrelia spp. antigenic variation at red cell surface in malaria and, 673, 678, 695

septicemia bacteriophage therapy and, 439, 445

Bradyrhizobium japonicum thiol-redox pathways and,

fatty acid antibiotics and,

Brownian motion big bacteria and, 107-8,

biological weapons and,

horizontal gene transfer in prokaryotes and, 720, 722 Budvicia spp.

coliform group bacteriology and, 206, 209, 216, 219, 221 Burkholderia spp. biological weapons and, 237 quorum sensing and, 174 **BURST** algorithm recombination and bacterial population structure, 576-78 Buttiauxella spp. coliform group bacteriology and, 206, 209, 215-19, 221 C c2-like genus dairy bacteria phages and, 283, 285, 295 Ca2+ fungal pathogenesis and, Caenorhabditis elegans horizontal gene transfer in prokaryotes and, 716, 726-28 Caephalosporium caerulens fatty acid antibiotics and, Campylobacter jejuni horizontal gene transfer in prokaryotes and, 716, 720, 726-28 quorum sensing and, 186 Candida albicans fungal pathogenesis and, 744-50, 752-58, 761-62 Candida spp. fungal pathogenesis and, 744, 747, 750-51, 754, 757-58 capBCA system anthrax and, 650, 652

car genes

periplasmic stress and

extracytoplasmic function sigma factors, 602, 606-8 cbpA gene polarized epithelium and pathogens, 414 ccmG gene thiol-redox pathways and, 36 Cedacea spp. coliform group bacteriology and, 206, 209 CEK1 gene fungal pathogenesis and, 752 Cell division bacterial gliding motility and, 66 Cell growth viruses and interferons, 273-74 Cell inclusions big bacteria and, 105 Cell polarity pathogenesis and, 407-25 Cell size prokaryote big bacteria and, 105-32 Cell wall dairy bacteria phages and, hydrophobins and, 625, 637-38

periplasmic stress and

Cell-mediated immunity

Mycobacterium

Cell-population density

quorum sensing and,

Centers for Disease Control

759-61

165-89

(CDC)

extracytoplasmic function

sigma factors, 591-617

fungal pathogenesis and,

nonreplicating latency of

tuberculosis and, 143

viral latency and, 538-39 Chemolitho-autotrophic bacteria ammonia-oxidizing, 485-517 Chemotaxis big bacteria and, 105, 111 - 13Chlamydia spp. antigenic variation at red cell surface in malaria and, 695 homology-dependent gene silencing in fungi and, 398 horizontal gene transfer in prokaryotes and, 709, 716, 719, 725-28, 736 polarized epithelium and pathogens, 417-19 Chlamydophyla spp. horizontal gene transfer in prokaryotes and, 719-20, 722, 724, 726-27 Chloramphenicol

biological weapons and,

79.83

CFTH1 gene

629

cglB gene

Chaperones

che genes

Chemokines

Cerulenin

toxic shock syndrome and,

fatty acid antibiotics and,

hydrophobins and, 626-27,

bacterial gliding motility

periplasmic stress and

extracytoplasmic function sigma factors, 594-95

bacterial gliding motility

immune checkpoints in

305-6, 313-14

and, 57-58

and, 57-59

Commuting

big bacteria and, 128, 130

Comparative genomics

bacteriophage therapy and, recombination and the bacterial species, 447 bacterial population 205-10 structure, 565, 570-71. Chlorine dioxide colonizers, 214-15 biological weapons and, 577, 583-85 conclusions, 223-24 244 Clones Escherichia coli, 220 Chlorochromatium spp. antigenic variation at red enteropathogenic group, cell surface in malaria big bacteria and, 119 213-14 environmental group, Chloroflexus aurantiacus and, 673-97 bacterial gliding motility recombination and 221 and, 68 bacterial population fecal, 211-13, 219-21 Cholera structure, 561, 563-65. fish, 218-19 bacteriophage therapy and, 567-73, 575-80, 583-85 from species to habitat, 440, 446 Clostridium botulinum 210-11 Chromatium spp. biological weapons and, insects, 218-19 big bacteria and, 119 236, 244 intestinal, 211-13 novel thiols and, 336 Clostridium spp. introduction, 202-3 Chromobacterium violaceum anthrax and, 651 markers, 221-23 quorum sensing and, 174 coliform group molluscs, 218-19 Chromosomes bacteriology and, 211-12, opportunistic pathogens, bacteriophage therapy and, 214-15 445 fatty acid antibiotics and, plants, 217-18 cl gene 309, 323 psychrotrophic group, dairy bacteria phages and, novel thiols and, 347 215-17 290 quorum sensing and, 186 rodents, 218-19 traditional classification. Citrobacter spp. Clusters of orthologous coliform group groups (COGs) 203-5 bacteriology and, 203, horizontal gene transfer in ubiquitous group, 205-8, 210, 212-13, prokaryotes and, 714-16 220-21 216-17, 220-23 Coccidioides immitis Colonizers Cladistics fungal pathogenesis and, coliform group 744-46, 751, 757 horizontal gene transfer in bacteriology and, 214-15 prokaryotes and, 718 hydrophobins and, 635 com genes novel thiols and, 342 symbiosis and Coenzymes B and M fungus-growing ants, 365 novel thiols and, 333, quorum sensing and. Cladosporium spp. 337-42 179-81 fungal pathogenesis and, Coevolution Commensals symbiosis and fungal pathogenesis and, fungus-growing ants, 357, 756 hydrophobins and, 626-27, 638-39 361-62 recombination and CLAG9 gene COH genes bacterial population antigenic variation at red hydrophobins and, 626-27. structure, 572 cell surface in malaria 639 Communication circuits and, 685 Cold-sensitive mutants quorum sensing and, Claviceps fusiformis history of research, 12-14 165-89

Coliform group

water safety and

changing designation of

hydrophobins and, 626-27,

629-30

Clonal complexes

dairy bacteria phages and, 285-89 ComP/ComA competence sporulation system quorum sensing and, 179-82 Competence quorum sensing and, 165, 179-82 Competitive advantage big bacteria and, 105 symbiosis and fungus-growing ants, 364 Complementation studies hydrophobins and, 625 Conjugation quorum sensing and, 165 Consensus model of latency immune checkpoints in viral latency and, 548-49 Coprinus cinereus hydrophobins and, 626-27,

639 Corvnebacterium spp. fatty acid antibiotics and, novel thiols and, 347

cos-site phages dairy bacteria phages and, 283, 285-89, 293-95

Cosuppression homology-dependent gene silencing in fungi and, 391-92

Coxiella burnetii biological weapons and, 236, 238

CPH1 gene fungal pathogenesis and, 752

cpx genes periplasmic stress and extracytoplasmic function sigma factors, 591-617

cro gene dairy bacteria phages and, 290

Cross-reactivity immunological antigenic variation at red cell surface in malaria and, 673, 680

Crv gene hydrophobins and, 626-27 Cryphonectria parasitica hydrophobins and, 626-27, 629, 634

Cryptococcus neoformans fungal pathogenesis and, 744-46, 749, 754-56, 760-61 csaAB operon

anthrax and, 654 CTO primers ammonia-oxidizing bacteria and, 496

Cu gene hydrophobins and, 626-27, 629, 631, 635-37, 639 cya gene

anthrax and, 650, 654 Cvanobacteria bacterial gliding motility and, 49, 60-62 big bacteria and, 116 Cyclogeny

bacteriophage therapy and, 442 Cyclosporin

periplasmic stress and extracytoplasmic function sigma factors, 595 Cyphomyrmex spp. symbiosis and

fungus-growing ants, 359 Cystic fibrosis quorum sensing and, 170 - 71

Cys-X-X-Cys sequence motif thiol-redox pathways and, 21-22, 25, 32

Cytoadherence antigenic variation at red cell surface in malaria

and, 673, 681, 683-89,

Cytochromes thiol-redox pathways and, 33-34

Cytokines immune checkpoints in viral latency and, 538-39 toxic shock syndrome and, 77, 85, 94 viruses and interferons. 255-75

Cytomegalovirus (CMV) immune checkpoints in viral latency and, 545-46 Cytophaga-Flavobacterium

group bacterial gliding motility and, 49-50, 62-66

Cytophaga hutchinsonii bacterial gliding motility and, 68

Cytoplasm big bacteria and, 105 periplasmic stress and extracytoplasmic function sigma factors, 592-93 thiol-redox pathways and, 21, 23-30, 37-39

## D

Dairy bacteria phages comparative genomics, 285-89 DNA packaging, 293-94 genetic switch, 290 head proteins, 294-95 integration/excision, 291-92 introduction, 284 introns, 290-91 Lactobacillus phages, 288-89 Lactococcus phages, 285-87 lysis cassette, 295-96 outlook, 296-97

replication, 292-93 Streptococcus phages, 287-88 tail proteins, 294-95 transcription, 289-90 "Death by exhaustion" concept nonreplicating latency of Mycobacterium tuberculosis and, 156 Decontamination biological weapons and, 235, 243-45 degP gene periplasmic stress and extracytoplasmic function sigma factors, 592. 594-96, 599, 602, 607-8, 611, 613-15 Deinococcus radiodurans horizontal gene transfer in prokaryotes and, 716, 720, 723, 726-28, 732, 735 Delisea pulchra quorum sensing and, 188 Denaturing gradient gel electrophoresis (DGGE) ammonia-oxidizing bacteria and, 496, 505, 509-10 Denitrification history of research, 15-16 dep gene anthrax and, 650 Desulfonema spp. big bacteria and, 130 Desulfovibrio sp. ammonia-oxidizing bacteria and, 510 Development hydrophobins and, 625-40 dewA gene hydrophobins and, 626-27 d'Herelle F

bacteriophage therapy and,

437-39, 441-46

Diazoborine fatty acid antibiotics and. 305-6, 319-22 Differential induction viruses and interferons. 260-61 Diffusion big bacteria and, 105, 107-11, 121-23 Diffusive boundary layer big bacteria and, 105, 114-15, 124-27 dif genes bacterial gliding motility and, 57, 59 Direct extraction ammonia-oxidizing bacteria and, 508-9 Dispersal biological weapons and, 235 Dissemination factors fungal pathogenesis and, Disulfide bonds thiol-redox pathways and, 21-40 Diversity ammonia-oxidizing bacteria and, 485, 492-505 DNA chip technology ammonia-oxidizing bacteria and, 511-12 **DNA** degradation homology-dependent gene silencing in fungi and, 381-82, 384-90, 397 **DNA-DNA** hybridization coliform group bacteriology and, 201, 205, 214 DNA packaging dairy bacteria phages and, 283, 287, 293-94 DNA polymerase II horizontal gene transfer in

prokaryotes and, 714-15 Dormancy nonreplicating latency of Mycobacterium tuberculosis and, 139-56 Double-stranded RNA (dsRNA) viruses and interferons. 255-58, 263-64, 275 Drinking water coliform group bacteriology and, 201-24 Drosophila melanogaster horizontal gene transfer in prokarvotes and, 716, 726-28 "Drug indifference" nonreplicating latency of Mycobacterium tuberculosis and. 140 Drug-resistant pathogenic bacteria fatty acid antibiotics and. 305-25 dsb genes periplasmic stress and extracytoplasmic function sigma factors, 594 thiol-redox pathways and, 31 - 36Duffy binding-like superfamily antigenic variation at red cell surface in malaria and, 687, 689 Dysentery bacteriophage therapy and,

E
eag gene
anthrax and, 653, 660
eas gene
hydrophobins and, 626–27
Ecology
ammonia-oxidizing

437-39

758

history of research, 9-12

fatty acid antibiotics and,

**Enoyl-ACP** reductase

ammonia-oxidizing

Entamoeba histolytica

bacteria and, 508-9

318-22

**Enrichments** 

Enology

bacteria and, 485-517 novel thiols and, 335 Enteric origins anthrax and, 662 antigenic variation at red coliform group cell surface in malaria bacteriology and, 201, and, 676 211 - 13big bacteria and, 119-30 Enterobacter spp. coliform group coliform group bacteriology and, 201-24 bacteriology and, 201, recombination and 203-8, 210, 212-23 bacterial population quorum sensing and, 174 structure, 562 Enterococcus spp. Economic factors coliform group biological weapons and, bacteriology and, 211-12, dairy bacteria phages and, quorum sensing and, 166, 283-97 186 Edema factor Envelope stress anthrax and, 657 periplasmic stress and Edwardsiella spp. extracytoplasmic function sigma factors, 591-617 coliform group bacteriology and, 206 **Environmental factors** EFG1 gene coliform group fungal pathogenesis and, bacteriology and, 201, 752 221 Electron acceptor **Epigenetics** homology-dependent gene big bacteria and, 105, 130-31 silencing in fungi and, 382-98 Electron transfer novel thiols and, 340 **Epizootic infections** thiol-redox pathways and, bacteriophage therapy and, 21, 23-24, 27, 32-37 437-48 Elicitors Epoxythane biological weapons and, hydrophobins and, 625, 637 244 quorum sensing and, 165 EPR gene Endogenous infection routes fungal pathogenesis and, 749 fungal pathogenesis and,

Epstein-Barr virus (EBV)

Epulopiscium fischeloni

Ergothioneine

346-49

Erwinia spp.

immune checkpoints in

big bacteria and, 105-6,

108, 110, 115-18, 131

novel thiols and, 333,

viral latency and, 546-47

coliform group bacteriology and, 206-8, 211, 215, 217-19, 221 quorum sensing and, 167, 172-74, 188 Erythrocytes antigenic variation at red cell surface in malaria and, 673-97 Erythromycin novel thiols and, 345 Escherichia coli ammonia-oxidizing bacteria and, 516 anthrax and, 652 bacterial gliding motility and, 52, 58 bacteriophage therapy and, 444-47 big bacteria and, 111, 117 biological weapons and, 247 coliform group bacteriology and, 201-24 dairy bacteria phages and, 292 fatty acid antibiotics and, 307-13, 315-16, 318-24 history of research, 8, 11, 15 horizontal gene transfer in prokaryotes and, 710-11, 714-16, 719-22, 726-28 nonreplicating latency of Mycobacterium tuberculosis and, 153 novel thiols and, 336-37, 342.347 periplasmic stress and extracytoplasmic function sigma factors, 591-617 polarized epithelium and pathogens, 411, 414-15 quorum sensing and, 174, 183, 186 recombination and bacterial population

structure, 562, 564-65. structure, 561, 567-68. 567-69, 578, 580, 583 570, 572, 580 thiol-redox pathways and, symbiosis and 21-40 fungus-growing ants, 357-75 Escovopsis spp. symbiosis and thiol-redox pathways and. fungus-growing ants, 357, 368-75 toxic shock syndrome and, 77, 86, 90 Estrogen-binding proteins fungal pathogenesis and, viruses and interferons. 255-58 757 Ethionamide Ewingella spp. fatty acid antibiotics and. coliform group bacteriology and, 206, 209 Ethylene oxide biological weapons and. Excision 244-45 dairy bacteria phages and, Eubacterium spp. 283, 291-92 coliform group Exogenous infection routes bacteriology and, 211-12 fungal pathogenesis and, 758-59 Euglena sp. big bacteria and, 112 Exosporium anthrax and, 651 Eukarvotes Exploitation ammonia-oxidizing bacteria and, 494 polarized epithelium and horizontal gene transfer in pathogens, 423-24 prokaryotes and, 709-12, Extracytoplasmic factors 714, 719, 733-36 anthrax and, 660 Euprymna scolopes Extracytoplasmic function quorum sensing and, (ECF) sigma factors periplasmic stress and 167 Eutrophication Bacillus subtilis oX and  $\sigma^{W}$ , 602-4, 614 ammonia-oxidizing bacteria and, 485 bacterial envelope,

Evasion

Evolution

269-72

viruses and interferons.

antigenic variation at red

cell surface in malaria

dairy bacteria phages and,

horizontal gene transfer in

prokaryotes and, 710-18

and, 695, 697

290, 296-97

recombination and

bacterial population

593-94

chaperones, 595

classification, 596-97

conclusions, 616-17

Cpx envelope stress

response, 606-12

discovery, 592-93

envelope biogenesis,

envelope protein

downstream targets, 599,

cytoplasm, 592

611-12

615-16

misfolding, 593-96 Escherichia coli o E. 602. 613-14 future research, 616-17 history, 592-93 inducing cues, 599-601. 608-9 miscellaneous **ECF-regulated stress** responses, 601, 603-6 Mycobacterium spp. SigE and SigH, 602. 604-5 Myxococcus xanthus CarQ, 602, 606-8 overlap in stress responses, 612-14 pathogenicity, 615-16 Pseudomonas aeruginosa algU, 601 - 3regulation, 597-98 responses to extracytoplasmic stress, 596-97 role of envelope stress responses, 614-16  $\sigma$  envelope stress response, 598-602  $\sigma^{E}$  homologues, 601 signal transduction, 599-601, 609-10 Streptomyces spp.  $\sigma^{E}$ , 602, 605 upregulation, 595-96 virulence, 615-16

fab genes fatty acid antibiotics and, 307-23 Facultative anaerobes anthrax and, 647-63 FAS2 gene fungal pathogenesis and, 748 Fast swimmers

big bacteria and, 105, big bacteria and, 123-24 frz gene 119-23, 126-31 bacterial gliding motility Fatty acid antibiotics and, 57, 59 acetyl-CoA carboxylase. symbiosis and 310-11 fungus-growing ants, 371, Functional genomics cerulenin, 313-14 ammonia-oxidizing conclusions, 324-25 Filamentous cyanobacteria bacteria and, 511-12 diazoborine, 319-22 bacterial gliding motility Fungi and, 49, 60-62 homology-dependent gene enovl-ACP reductase, 318-22 Filamentous fungi silencing and, 381-98 hydrophobins and, 625-40 inhibitors, 318-22 fungal pathogenesis and, 754-55 pathogenesis and enzymes, 307-24 homology-dependent gene adaptations of specific genes, 308-9 3-hydroxyacyl-ACP silencing in fungi and. organisms, 754-55 382-86, 389-91 adherence, 746-47 dehydrase, 317 calcium, 755 initiation of fatty acid hydrophobins and, 625-40 synthesis, 309-10 fimS gene cell-mediated immunity. introduction, 305-7 bacterial gliding motility 759-61 3-ketoacyl-ACP reductase, and, 53 classes of infections. 761-63 316-17 Firmicutes spp. horizontal gene transfer in conclusions, 763 3-ketoacyl synthases I. II. and III. 312-16 prokaryotes and, 719 dissemination factors. inhibitors, 313-16 748 fkpA gene endogenous infection malonyl-CoA:ACP periplasmic stress and extracytoplasmic function transacylase, 311 routes, 758 "missing" enzymes, sigma factors, 594-95. estrogen-binding proteins, 757 322-24 peripheral enzymes as Flavobacterium johnsoniae exogenous infection bacterial gliding motility routes, 758-59 targets, 324 proteins, 307-24 and, 50-51, 58, 64-66 host reponse, 756-61 thiolactomycin, 314-16 Flexibacter filiformis humoral immunity, 759 triclosan, 318-19 bacterial gliding motility iatrogenic factors, 758 and, 58, 62 immunocompetence, FBH1 gene hydrophobins and, 626-27 Flowing water 757 - 58big bacteria and, 119-21 infecting agent, 744-45 fdxA gene novel thiols and, 345 Formaldehyde introduction, 744 Feces biological weapons and, iron, 755 coliform group 244-45 mating type, 756 bacteriology and, 201, Francisella tularensis melanin, 755 211-13, 219-21 biological weapons and, metabolic factors. Fermentation 236, 238 748-49 Free radicals milk morphology, 751-54 dairy bacteria phages biological weapons and, multiple parasitic cell and. 283-97 245 forms, 752-53 "Free-wheeling" necrotic factors, 749-51 Fever toxic shock syndrome and, antigenic variation at red nutritional factors, 748 77, 80, 82 cell surface in malaria opportunistic pathogens, Filamentous bacteria and, 678 745

penetration factors, 748 dairy bacteria phages and, gerX gene pH, 754 283, 285 anthrax and, 649-50 phenotypic switching, Gene displacement Giardia spp. 753-54 xenologous antigenic variation at red platelets, 761 horizontal gene transfer cell surface in malaria primary pathogens, 745 in prokarvotes and. and, 695 specific parasitic cell 709, 718, 727, 734-36 novel thiols and, 335 forms, 751-52 Gene silencing old genes surface properties. homology-dependent bacterial gliding motility 755-56 fungi and, 381-98 and, 51, 64-67 temperatures, 746 Generalist pathogens Gliding motility toxins, 754-55 symbiosis and bacterial, 49-69 underlying disease, fungus-growing ants, Gliotoxin 757-58 369-70 fungal pathogenesis and, virulence factors. Genetic mapping 754 745-56 dairy bacteria phages and, Global cycling Fungus-growing ants 283, 287 of nitrogen symbiosis and, 357-75 Genetic switch ammonia-oxidizing Fusarium spp. dairy bacteria phages and, bacteria and, 485, biological weapons and, 283, 287, 290 488-89 Genital mucosa Global warming fungal pathogenesis and, polarized epithelium and novel thiols and, 338 758, 762 pathogens, 417 Glucosamine Fusel oil "Genome hypothesis" novel thiols and, 333 history of research, 11-12 horizontal gene transfer in y-Glutamylcysteine prokaryotes and, 717 novel thiols and, 333, 337 "Genomescape" Glutaredoxin G75 thiol-redox pathways and, horizontal gene transfer in fatty acid antibiotics and. prokaryotes and, 711 21, 26-28 306 Genomics Glutathione (GSH) B-Galactosidase novel thiols and, 335-37, ammonia-oxidizing 343-44, 348 coliform group bacteria and, 511-12 bacteriology and, 201-24 antigenic variation at red thiol-redox pathways and, Gamma herpes virus 26-28 cell surface in malaria viruses and interferons, and, 673, 689-91 Glutathione amide 269 novel thiols and, 333 coliform group garB gene bacteriology and, 201-24 Glutathione reductase novel thiols and, 336 dairy bacteria phages and, thiol-redox pathways and, 283, 285-89, 296-97 26-28 Gardens Glutathionylspermidine symbiosis and homology-dependent gene fungus-growing ants, silencing in fungi and. novel thiols and, 336-37 357-75 395-98 Glyceria maxima Gene acquisition horizontal gene transfer in ammonia-oxidizing horizontal gene transfer prokaryotes and, 711-13 bacteria and, 503 in prokaryotes and, Gerronema spp. Gonococci 709, 734 symbiosis and polarized epithelium and Gene clusters fungus-growing ants, 361 pathogens, 417-18

gor gene thiol-redox pathways and, 37-39 Gram-negative bacteria ammonia-oxidizing bacteria and, 492 novel thiols and, 347 quorum sensing and, 165, 167-77 Gram-positive bacteria anthrax and, 647-63 dairy bacteria phages and, horizontal gene transfer in prokaryotes and, 719 novel thiols and, 347-48 quorum sensing and, 165, 177-82 Growth factors viruses and interferons. 255-58 grxA gene thiol-redox pathways and, 24-25, 27 gsh genes novel thiols and, 337 thiol-redox pathways and, 27 Haemophilus ducrevi fatty acid antibiotics and, 322 Haemophilus influenzae fatty acid antibiotics and, 322 horizontal gene transfer in prokaryotes and, 711, 716, 719-20, 722-23, 726-28, 735 quorum sensing and, 186 recombination and bacterial population structure, 581-82 Hafnia spp.

coliform group

bacteriology and, 206-8, 211 Halobacteria aerobic phototrophic novel thiols and, 333. 337, 348 Halobacterium spp. horizontal gene transfer in prokaryotes and, 720-21. 726-28 novel thiols and, 338 hcf genes hydrophobins and, 626-27 Head and tail morphogenesis dairy bacteria phages and, 283, 294-95 "Headful" mechanism dairy bacteria phages and, Head proteins dairy bacteria phages and, 294-95 Helicobacter pylori horizontal gene transfer in prokaryotes and, 716, 720, 728 polarized epithelium and pathogens, 415 quorum sensing and, 186 recombination and bacterial population structure, 569, 584 thiol-redox pathways and, 26 hemA gene thiol-redox pathways and, 32 Heptamerization anthrax and, 647, 655 Herpesviruses immune checkpoints in viral latency and, 531-34, 544-47 viruses and interferons. 269 Heterotrophic bacteria ammonia-oxidizing

bacteria and, 513-14 big bacteria and, 105 Hfb genes hydrophobins and, 626-27 High-efficiency particulate air (HEPA) filters biological weapons and, Histoplasma capsulatum fungal pathogenesis and, 744, 746, 748, 751, 754-55, 760 hld gene quorum sensing and, 181 Homeostasis immune checkpoints in viral latency and, 531-53 Homology-dependent gene silencing (HDGS) fungi and Ascobolus immersus, 384-86 cosuppression, 391-92 genome-protective mechanism, 395-98 methylation induced premeiotically, 384-86 Neurospora crassa, 382-84, 390-91 Phytophthora infestans, 386-87 plants, 391-92 posttranscriptional gene silencing, 390-95 quelling, 390-91 repeat-induced point mutations, 382-84 RNA interference. 392-93 similarities and differences between transcriptional gene silencing in plants and fungi, 387-88 transcriptional gene silencing, 382-90 transnuclear

transcriptional gene silencing, 386-87 Homo sapiens horizontal gene transfer in prokaryotes and, 726-27 Homoserine lactones acetylated quorum sensing and, 165, 170-77, 183-85, 188 Horizontal gene transfer in prokaryotes aminoacyl t-RNA synthetases, 729, 732 - 33anomalous nucleotide composition, 717 archaea, 723-35 bacteria, 723-35 classification, 718-35 conclusions, 735-36 conservation of gene order between distant taxa, 715, 717 criteria for detection of horizontally transferred genes, 713-17 establishing direction, 717 - 18eukaryotes, 723-35 introduction, 710-12 miscellaneous eukaryotic genes acquired by prokaryotes, 733-35 operons, 715, 717 quantification, 718-35 unexpected phylogenetic tree topology, 713-14 unexpected ranking of sequence similarity among homologs, 713 unusual phyletic patterns, 714-16 Host immunity toxic shock syndrome and, 85-86

Housekeeping genes recombination and bacterial population structure, 561, 567, 572, 578 Hum2 gene hydrophobins and, 626-27 Human immunodeficiency virus (HIV) immune checkpoints in viral latency and, 531-32, 536, 547-48 Humoral immunity antigenic variation at red cell surface in malaria and, 673-97 fungal pathogenesis and, 759 HWP1 gene fungal pathogenesis and, Hybrid homoserine lactone/two component signaling circuit quorum sensing and, 183-85 Hyd genes hydrophobins and, 626-27 Hvd-Pt genes hydrophobins and, 626-27 Hydrogen peroxide biological weapons and, Hydrogen sulfide big bacteria and, 105-32 Hydrophobins attachment, 635-37 coating air-exposed fungal surfaces, 634-35 conclusions, 640 functions, 638-40 hyphal escape from aqueous environment,

630-34

Host-range specificity

443

bacteriophage therapy and,

hyphal wall composition, 637-38 interfacial self-assembly, 628-30 introduction, 625-28 pathogenicity, 635-37 toxins, 637 3-Hydroxyacyl-ACP dehydrase fatty acid antibiotics and, 317 HYPA gene hydrophobins and, 626-27 Hyperthermophiles horizontal gene transfer in prokaryotes and, 709, 711 Hyphae fungal pathogenesis and, 748, 752, 761 hydrophobins and, 625, 630-34, 639-40 Hypotension toxic shock syndrome and, 77, 79-80 Hypoxia nonreplicating latency of Mycobacterium tuberculosis and, 139, 145-55

Illegitimate recombination recombination and bacterial population structure, 563, 567-68 Immune checkpoints viral latency and adaptive immune response, 540-41 apoptosis inhibitors. 539-40 CD4 memory, 536 CD8 memory, 535 chemokine homologues, 538-39 conclusions, 551-53 consensus model of

latency, 548-49	biological weapons and,	differential induction of
cytokine homologues,	235, 245-49	IFN-α, 260–61
538–39	Indels	dsRNA-stimulated gene
cytomegalovirus, 545–46	dairy bacteria phages and, 287	induction, 263-64 future research, 274-75
Epstein-Barr virus, 546-47	Indicator organisms ammonia-oxidizing	gamma herpes virus, 269
herpesvirus, 544–47 HIV, 547–48	bacteria and, 515–16 Inducing cues	IFN- $\beta$ induction, 259–60
HSV-1, 544-45	periplasmic stress and	IFN-γ induction, 261
immune surveillance, 549–51	extracytoplasmic function sigma factors, 599-601,	IFN-induced proteins, 264-67
immune thresholds, 549-51	608–9 Influenza virus	immune system cells, 273
innate immune response, 532–33, 537–40	viruses and interferons, 268 Ingraham JL, 1–16	influenza virus, 268 introduction, 256–58
introduction, 532	inhA gene	Mx, 266
memory T-cell	fatty acid antibiotics and,	P56, 265–66
responses, 535	320–22	P200 family, 266
MHC class I and II antigen presentation,	Innate immune response immune checkpoints in	picorna viruses, 268 PKR, 265
541–44 naïve T-cell responses,	viral latency and, 531, 537-40	properties of IFNs, 258-59
535–36	int genes	receptors, 261
natural killer cells, 537–38	dairy bacteria phages and,	regulatory factors, 259–61, 266–67
viral	fungal pathogenesis and,	STAT1, 263
immunomodulation,	747, 752	Thogoto virus, 268
536-44	toxic shock syndrome and,	type I IFN signaling,
Immune evasion	88–89	261–62
antigenic variation at red	Integration/excision	type II IFN signaling,
cell surface in malaria	dairy bacteria phages and,	262-63
and, 673, 679–80	283, 291–92	vesicular stomatitis
immune checkpoints in	Interfacial self-assembly	virus, 268–69
viral latency and, 531, 536 Immunology	hydrophobins and, 628–30 Interferons (IFNs)	viral evasion of IFN system, 269–72
bacteriophage therapy and,	viruses and	Interspecies communication
444-45	2-5(A) synthetase/Rnase	quorum sensing and,
fungal pathogenesis and,	L, 264-65	185–86
757–58	antiviral actions, 267-69	Intestines
toxic shock syndrome and, 77, 85–86	block in signaling, 270–71	coliform group bacteriology and, 211-13
		Intravenous immunoglobulin
vector biology of leishmaniasis and, 473–75	block in synthesis, 270 cell growth, 273–74	
	classification of IFNs,	(IVIG)
viruses and interferons, 273	258–59	toxic shock syndrome and, 85-86
Incident response	clinical use, 274	Introns

dairy bacteria phages and, 290-91 Iron fungal pathogenesis and, 755 Isoleucyl aminoacyl-tRNA synthetases horizontal gene transfer in prokaryotes and, 709, 729, 732-33, 736 Isoniazid fatty acid antibiotics and, 305-6 nonreplicating latency of Mycobacterium tuberculosis and, 144 Jak-STAT pathways viruses and interferons. 255-58, 261-63, 270-71, 274 Junctional pores bacterial gliding motility and, 61 K KAHRP gene antigenic variation at red cell surface in malaria and, 684-85 kasA gene fatty acid antibiotics and, 320, 322 kat genes fatty acid antibiotics and, "Keep them from awakening" concept nonreplicating latency of Mycobacterium tuberculosis and, 156 3-Ketoacyl-ACP reductase fatty acid antibiotics and,

316-17

and III

3-Ketoacyl synthases I, II,

fatty acid antibiotics and. quorum sensing and. 312-16 168-71 "Kill them as they sleep" Latency concept nonreplicating latency of nonreplicating latency of Mycobacterium tuberculosis and, 156 viral Klebsiella spp. coliform group bacteriology and, 203-7, Lateral genomics 208, 210-13, 215-17, 219-23 quorum sensing and, 186 lecA gene Kluyvera spp. Leclercia spp. coliform group bacteriology and, 206, 209, 218 Knobs antigenic variation at red lef gene cell surface in malaria and, 684, 696 Koch R. 647 L Lactic acid 471-72 dairy bacteria phages and, 283-97 Lactobacillus spp. coliform group bacteriology and, 211-12 dairy bacteria phages and. 283, 286, 288-97 458-59 novel thiols and, 347 Lactococcus spp. dairy bacteria phages and, 283, 285-88, 290-92, 473-75 296-97 thiol-redox pathways and, 459-60 28 lacZ operon periplasmic stress and

extracytoplasmic function

dairy bacteria phages and,

sigma factors, 599

Lambdoid coliphages

283, 287

las genes

Mycobacterium tuberculosis and, 139-56 immune checkpoints and, 531-53 horizontal gene transfer in prokarvotes and, 711 quorum sensing and, 170 coliform group bacteriology and, 206, 209, 215, 219, 221 anthrax and, 650, 654 Leishmania-sand fly interactions vector biology and anterior migration. attachment to midgut epithelial cells, 465-66 development of transmissible infections, 454-57 digestive enzymes. escape from peritrophic membrane, 464-65 immunomodulation. inhibition of midgut in infected sand flies. introduction, 454 LPG, 465-66 maturation of transmissible infections, 469-73 midgut receptors for parasite attachment. 468-69

parasite molecules controling early survival, 460-61 parasite mutants, 461-63 persistence of Leishmania following bloodmeal excretion. 463-69 potential barriers to complete development of transmissible infections, 457-58 presensitization, 475 sand fly saliva, 473-75 species-specific midgut attachment, 466-68 stage differentiation. 471-72 stage-specific midgut attachment, 469-71 survival in blood-fed midgut, 458-63 timing of the loss of infection in refractory sand flies, 463-64 transmission by bite. 472-73 Leminorella spp. coliform group bacteriology and, 206 Lentinula edodes hydrophobins and, 626-27 Leptospirillum spp. ammonia-oxidizing bacteria and, 494

Lethal factor anthrax and, 657 Lethal shock toxic shock syndrome and, 77–94

77–94
Leucoagaricus spp.
symbiosis and
fungus-growing ants, 361
Leucocoprinus spp.
symbiosis and
fungus-growing ants, 361
Levinea spp.

coliform group bacteriology and, 205 Lincomycin novel thiols and, 345 Linkage disequilibrium recombination and bacterial population structure, 561, 569-73 Listeria monocytogenes dairy bacteria phages and, polarized epithelium and pathogens, 420-21 lmbE gene novel thiols and, 345 LolA/p20LolB shuttle protein periplasmic stress and extracytoplasmic function sigma factors, 594 Ltx1 gene anthrax and, 657 luxCDABE operon quorum sensing and,

Lyngbya majuscula big bacteria and, 117 Lysis cassette dairy bacteria phages and, 295–96 Lysogeny

168-77, 183-86

bacteriophage therapy and, 445 dairy bacteria phages and, 286–87

### M

Macromonas mobilis

big bacteria and, 117
Madin-Darby canine kidney
(MDCK) cells
polarized epithelium and
pathogens, 412
Mag gene
hydrophobins and, 626–27

Magnaporthe griseae hydrophobins and, 626–27, 634, 636, 639 Magnetobacterium spp. ammonia-oxidizing bacteria and, 494 big bacteria and, 117 Major histocompatibility complex (MHC) immune checkpoints in viral latency and, 541–44 toxic shock syndrome and, 90–93

Malaria antigenic variation at red cell surface in, 673–97 Malolactic fermentation history of research, 10–11

Malonyl-CoA:ACP transacylase fatty acid antibiotics and, 311

marA gene fatty acid antibiotics and, 319

Marine environments ammonia-oxidizing bacteria and, 503-4

Marker organisms coliform group bacteriology and, 221–23 MATα genotype

fungal pathogenesis and, 756

Mating type fungal pathogenesis and, 756

Maximum likelihood tree recombination and bacterial population structure, 581–82

M cells polarized epithelium and pathogens, 411–12

Melanin fungal pathogenesis and, 755

Memory immune checkpoints in

viral latency and, 531, 533-53 menA gene thiol-redox pathways and, 2-Mercaptoethane sulfonic acid novel thiols and, 333, 337-42 7-Mercaptoheptanoylthreonine phosphate novel thiols and, 333. 337-42 Merthiolate bacteriophage therapy and, Mesophiles history of research, 8 Messenger RNA (mRNA) sequence-specific degradation homology-dependent gene silencing in fungi and. 381-82, 390-96 Metabacterium polyspora big bacteria and, 118 Metabolism fungal pathogenesis and, 748-49 novel thiols and, 333-49 Metalloproteases anthrax and, 647, 657 Metarhizium anisopliae hydrophobins and, 626-27, 636 metE gene thiol-redox pathways and, Methanobacterium spp. horizontal gene transfer in prokaryotes and, 716, 719-20, 723, 726-28 novel thiols and, 337, 341

Methanococcus jannaschii

726-27

horizontal gene transfer in

prokaryotes and, 720,

novel thiols and, 342 thiol-redox pathways and, Methanogens novel thiols and, 333. 338-42 Methanosarcina barkeri novel thiols and, 339-41 Methanosarcina mazei novel thiols and, 339-40 Methicillin recombination and bacterial population structure, 577 Methionine sulfoxide reductase thiol-redox pathways and, 29-30, 38 Methylation induced premeiotically (MIP) homology-dependent gene silencing in fungi and. 384-86 mglA gene bacterial gliding motility and, 59 Microarrays ammonia-oxidizing bacteria and, 512 Microbial ecology ammonia-oxidizing bacteria and, 485-517 Milk fermentation industrial dairy bacteria phages and, 283-97 "Missing" enzymes fatty acid antibiotics and, 322-24 mitC gene novel thiols and, 345 Mitogen-activated protein kinases (MAPKKs) anthrax and, 647, 657-58 Mitomycin

novel thiols and, 345

Mitomycin C

dairy bacteria phages and, 290 toxic shock syndrome and, Moellerella spp. coliform group bacteriology and, 206, 209 Monocentris japonicus quorum sensing and, 167 Monocultures symbiosis and fungus-growing ants, 366-67 Monomerization hydrophobins and, 625, 633 Monomorphism anthrax and, 662-63 Morganella spp. coliform group bacteriology and, 206 Morphogenetic proteins hydrophobins and, 625-40 MPG1 gene hydrophobins and, 626-27, 636, 639 msh genes novel thiols and, 346 mtr gene novel thiols and, 344 Mucosal fungal infections fungal pathogenesis and, 743, 761-62 Multichannel Lux circuit quorum sensing and, 183-85 Multicopy, nonallelic gene families antigenic variation at red cell surface in malaria and, 673, 687-96 Multilocus enzyme electrophoresis (MLEE) recombination and

bacterial population

structure, 564-72, 574, 583-85 Mycobacterium spp. Multilocus sequence typing (MLST) recombination and bacterial population structure, 561, 574-80, 582-85 Multiple-locus VNTR analysis (MLVA) anthrax and, 663 Multiple organ failure of toxic shock syndrome and, 77.79 Mutualism symbiosis and fungus-growing ants, 357-75 Mx protein viruses and interferons, 142-46 266, 268 Mycetarotes spp. 148-49 symbiosis and fungus-growing ants, 359 Mycetophylax spp. symbiosis and fungus-growing ants, 359 Mycetosoritis spp. symbiosis and 154 fungus-growing ants, 359 Mycobacteria dairy bacteria phages and, 283, 286 novel thiols and, 347 Mycobacterium bovis 148-49 fatty acid antibiotics and, 316 152-54 novel thiols and, 343 recombination and bacterial population 148-49 structure, 584

Mycobacterium leprae

316, 318, 321

23

thiol-redox pathways and,

Mycobacterium smegmatis fatty acid antibiotics and.

novel thiols and, 344-46 horizontal gene transfer in prokarvotes and, 735 Mycobacterium tuberculosis fatty acid antibiotics and, 316, 318, 320-22 horizontal gene transfer in prokaryotes and, 716. 720, 724, 726-28 nonreplicating persistence alternative energy sources, 149-51 biochemistry, 145-46 culture dynamics, 146 drug-induced Cornell mouse model, 144-45 experimental animals. future research, 155-56 genetic regulation, human host, 141-42 in vitro models of hypoxic NRP, 146-55 introduction, 140 macrophage cultures, "old stationary" models, optical density curves, phenotypic expression, regulatory factors. restriction of biosynthetic activities, slowly stirred, limited head space ratio (0.5 HSR) model, 147 stabilization and protection of essential products, 151-52 unstirred model, 146

untreated mouse model. 143-44 novel thiols and, 343-44, 346 quorum sensing and, 186 recombination and bacterial population structure, 564, 575, 583-84 Mycocepurus spp. symbiosis and fungus-growing ants, 359, 370 Mycoplasma genitalium horizontal gene transfer in prokaryotes and, 719, 721-22 Mycoplasma pneumoniae big bacteria and, 117 horizontal gene transfer in prokaryotes and, 719-20, 722 Mycoplasma spp. bacterial gliding motility and, 49, 67-68 Mycothiol novel thiols and, 333, 343-46 Mvo-inositol novel thiols and, 333, 345 Myoviridae dairy bacteria phages and, 289, 297 Myrmicocrypta spp. symbiosis and fungus-growing ants, 359,

370, 372

Myrotecium spp.

236

Myxobacteria

and, 54-59

Myxococcus fulvus

Myxococcus xanthus

and, 58

biological weapons and,

bacterial gliding motility

bacterial gliding motility

bacterial gliding motility and, 49–60, 67–68 periplasmic stress and extracytoplasmic function sigma factors, 596, 602, 606–8 quorum sensing and, 166–67, 186–87

## N

Naïve states immune checkpoints in viral latency and, 531, 533–37
Nanobacteria big bacteria and, 105–6
Natural killer (NK) cells immune checkpoints in viral latency and, 537–38 ndh gene fatty acid antibiotics and, 320–21

Neck passage structure dairy bacteria phages and, 294

Necrotic factors fungal pathogenesis and, 749-51

Neisseria gonorrhoeae bacterial gliding motility and, 50, 52, 54 polarized epithelium and pathogens, 417 recombination and bacterial population structure, 569, 584

Neisseria meningitidis
bacterial gliding motility
and, 54
biological weapons and,
237
horizontal gene transfer in
prokaryotes and, 716.

720, 722, 726–28 quorum sensing and, 186 recombination and bacterial population structure, 561, 570-73, 575, 578, 580-82

Neisseria spp. antigenic variation at red cell surface in malaria and, 673, 695

Neurospora crassa homology-dependent gene silencing in fungi and, 382–84, 389–91 hydrophobins and, 626–27, 634

novel thiols and, 347 Nitrate

big bacteria and, 105–32 Nitrobacter spp. ammonia-oxidizing bacteria and, 500, 503,

513 Nitrosococcus oceani ammonia-oxidizing bacteria and, 503, 513

Nitrosoguanidine history of research, 15 Nitrosomonas spp.

ammonia-oxidizing bacteria and, 485, 493–96, 498–99, 501–7, 509, 511, 514–16

Nitrospira spp. ammonia-oxidizing bacteria and, 485, 493–96, 498–507, 509, 514, 516

Nocardia spp. fatty acid antibiotics and, 314 novel thiols and, 347

Nonhomologous recombination recombination and bacterial population structure, 563, 567–68

Nonreplicating persistence Mycobacterium tuberculosis and, 139–56 Nonvariant parasite proteins antigenic variation at red cell surface in malaria and, 684-85 Norvaline history of research, 11-12 Nostoc punctiforme bacterial gliding motility and, 68

## O

Obesumbacterium spp.
coliform group
bacteriology and, 206
One-dimensional opposed
diffusion gradients
big bacteria and, 121–23
Opal gene
fungal pathogenesis and,
749

Ophiostoma novo-ulmi hydrophobins and, 626–27, 631, 635–37

Ophiostoma ulmi hydrophobins and, 626–27, 629, 631, 635–37

Opportunistic pathogens coliform group bacteriology and, 214–15 fungal pathogenesis and, 743, 745, 761 polarized epithelium and

pathogens, 423–24
Optical density curves
nonreplicating latency of
Mycobacterium
tuberculosis and, 148

Organized communities big bacteria and, 123–24 Orthologs

horizontal gene transfer in prokaryotes and, 709, 714–16

Oscillatoria spp. big bacteria and, 116

Oscillin bacterial gliding motility and, 61

Outer-membrane proteins

244

**Paralogs** 

periplasmic stress and horizontal gene transfer in extracytoplasmic function sigma factors, 593-95 extracytoplasmic function prokaryotes and, 709, sigma factors, 591-617 718, 734-35 Periplasm thiol-redox pathways and, "Out of Africa" principle Parasite-vector interactions leishmaniasis and, 453-75 21, 30-37 horizontal gene transfer in prokaryotes and, 718 **Parasites** Persistence antigenic variation at red nonreplicating Oxidative stress cell surface in malaria Mycobacterium ammonia-oxidizing bacteria and, 485-517 and, 673-97 tuberculosis and, 139-56 big bacteria and, 105-32 horizontal gene transfer in novel thiols and, 334-35 prokaryotes and, 709, 736 Personal protection thiol-redox pathways and, symbiosis and biological weapons and, 235, 241-43 21 - 22fungus-growing ants, 357, Oxygen 368-75 Peyer's patches big bacteria and, 105-32 Pasteur L, 647, 650 polarized epithelium and Pasteurella multocida pathogens, 411-12 OxyR transcription factor thiol-redox pathways and, bacteriophage therapy and, Pf60 family 25 439 antigenic variation at red Pathogenicity cell surface in malaria and, 693-95 periplasmic stress and P56 protein extracytoplasmic function PfEMP-1 viruses and interferons, sigma factors, 591-617 antigenic variation at red 265-66 polarized epithelium and, cell surface in malaria P200 protein family 407-25 and, 673, 679, 684-85, viruses and interferons, 266 symbiosis and 687-89, 691, 697 fungus-growing ants, 357, pac-site phages pH dairy bacteria phages and, 367-75 fungal pathogenesis and, 283, 285-86, 288, 294-95 Pathogenicity islands 750, 754, 760 toxic shock syndrome and, nonreplicating latency of pagA gene 89-90 Mycobacterium anthrax and, 650, 654, 659 Pantoea spp. Péclet number tuberculosis and, 140 coliform group big bacteria and, 110, 124 Phenol Pelochromatium spp. bacteriophage therapy and, bacteriology and, 206, 209, 215, 217-19, 221 big bacteria and, 119 443 Phenotypic switching PAPS reductase Penetration factors thiol-redox pathways and, fungal pathogenesis and, fungal pathogenesis and, 28-30, 38-39 748 753-54 Paracoccidioides brasiliensis Penicillin Phialocladus spp. recombination and fungal pathogenesis and, symbiosis and 757 bacterial population fungus-growing ants, 370 "Paracolon" forms Phlebotomine flies structure, 584 coliform group Peptide capsule vector biology and, 453-75 bacteriology and, 204 anthrax and, 647-48, Phormidium spp. Paraformaldehyde 651 - 52bacterial gliding motility biological weapons and, Peptidyl-prolyl isomerases and, 50, 61

(Ppiases)

periplasmic stress and

Phosphorylation

periplasmic stress and

extracytoplasmic function homology-dependent gene virulence, 681-87 sigma factors, 591-617 silencing in fungi and, fatty acid antibiotics and, Photorhabdus spp. 381, 387-88, 391-92 316 **Plasmids** coliform group Plasmodium spp. bacteriology and, 206 anthrax and, 650-51, biological weapons and. PHR genes 662-63 fungal pathogenesis and, Plasmodium falciparum **Platelets** 754 antigenic variation at red fungal pathogenesis and, Phylogenetic analysis cell surface in malaria and 761 ammonia-oxidizing antigenic variation in PLB1 gene bacteria and, 492-97 other pathogens, fungal pathogenesis and, anthrax and, 647, 662 695-96 750-51 horizontal gene transfer in antivariant antibodies in Pleurotus ostreatus prokaryotes and, 709-36 protection, 679-80 hydrophobins and, 626-27, recombination and background, 674 638-39 bacterial population cytoadherence, 684-87 pmoA gene structure, 561, 566-69, encoding domains with ammonia-oxidizing 580-83 defined adhesion bacteria and, 506 toxic shock syndrome and, properties, 688-89 Pneumococcus spp. 88 genetics, 687-95 polarized epithelium and Phytophthora infestans genomics, 689-91 pathogens, 410, 413-14 homology-dependent gene history, 676-77 Pneumocystis carinii silencing in fungi and, immune evasion, 679-80 antigenic variation at red 386-87 life cycle, 675-76 cell surface in malaria Picorna viruses major variant antigen and, 695 viruses and interferons, 268 genes, 686-88 fungal pathogenesis and, pil genes malaria models, 674-75 756, 758, 760 bacterial gliding motility modified red cell POH genes and, 53-56, 60 proteins, 685-86 hydrophobins and, 626-27, Pili 639 molecular genetics, type IV 687-95 Polarized epithelium bacterial gliding motility multigene families, bacterial pathogens and and, 49-69 693-95 apical membrane. Pilus assembly nonvariant parasite 414-17 periplasmic stress and proteins, 684-85 apical receptor, 413-14 basolateral membrane, extracytoplasmic function Pf60, 694-95 sigma factors, 591-617 reasons for antigenic 424-25 Pisolithus tinctorius variation, 696-97 Chlamydia spp., 418-19 hydrophobins and, 626-27 rif, 693, 694 Chlamydia trachomatis, PKR protein size of variant repertoire, 679 viruses and interferons. enteropathogenic 265, 272-73 Escherichia coli, stevor, 694 Plantomycetales surface antigen proteins, 414-15 exploitation, 423-24 ammonia-oxidizing 677-78 bacteria and, 487, 492, switching, 678-79, future research, 425 494 692-93 gonococci, 417-18 **Plants** var genes, 688-93 Helicobacter pylori, 415

introduction, 408–9	ammonia-oxidizing	extracytoplasmic function sigma factors, 594
	dacteria and, 493,	
		Pragia spp.
		coliform group
		bacteriology and, 206
		Primary pathogens
1-1	hydrophobins and, 628	fungal pathogenesis and,
		743–45
		Primers
	Polymorphism concept	ammonia-oxidizing
1000 00		bacteria and, 493–97,
	· · · —	509–10
		Probes
	bacterial gliding motility	ammonia-oxidizing
417		bacteria and, 493-97,
opportunistic pathogen,		509-10
423-24		Processed oligopeptides
overview, 409-11	441–44	quorum sensing and, 165,
paracellular route,	Population structure	177-82
424-25	bacterial	Prochloron sp.
	age of clonal complexes,	big bacteria and, 117
	583-85	Prokaryotes
	clonal diversification,	big bacteria and, 105-32
gingivalis, 424-25	575-80	coliform group
Pseudomonas	clones, 563-85	bacteriology and, 201-24
aeruginosa, 423-24	conclusions, 585	horizontal gene transfer
receptors, 414-15	Escherichia coli, 568-69	and, 709-36
Salmonella spp., 416-17	introduction, 562-63	novel thiols and, 333-49
Shigella spp., 419-20	linkage disequilibrium,	Prolate heads
specific	569-73	dairy bacteria phages and,
pathogen-epithelial cell	multilocus sequence	283
interactions, 413-25		Prophylaxis
Streptococcus		bacteriophage therapy and,
	570-73	437
	nucleotide sequence	Propionibacterium spp.
		novel thiols and, 347
transcytosis, 413-14		Propylene
		novel thiols and, 341
		Propylene glycol
	polarized epithelium and	biological weapons and,
	pathogens, 424–25	244
	Posttranscriptional regulation	Propylene oxide
	homology-dependent gene	biological weapons and,
		244
		Proteasome
		anthrax and, 657
(PCR)	periplasmic stress and	Protein folding
	overview, 409–11 paracellular route, 424–25 Peyer's patches, 411–12 pneumococci, 413–14 Porphyromonas gingivalis, 424–25 Pseudomonas aeruginosa, 423–24 receptors, 414–15 Salmonella spp., 416–17 Shigella spp., 419–20 specific pathogen-epithelial cell	in vitro tissue culture models, 412–13 ligands, 414–15 Listeria monocytogenes, 420–21 M cells, 411–12 MDCK cells, 412 miscellaneous cell lines, 412–13 mucosal pathogens of genital tract, 417 Neisseria gonorrhoeae, 417 opportunistic pathogen, 423–24 overview, 409–11 paracellular route, 424–25 Peyer's patches, 411–12 pneumococci, 413–14 Porphyromonas gingivalis, 424–25 Pseudomonas aeruginosa, 423–24 receptors, 414–15 Salmonella spp., 416–17 Shigella spp., 419–20 specific pathogen-epithelial cell interactions, 413–25 Streptococcus pneumoniae, 413–14 summary, 425 tight junctions, 424–25 transcytosis, 413–14 Yersinia spp., 421–23 lutants ummonia-oxidizing bacteria and, 515 yglutamic capsule untiphagocytic anthrax and, 647–48, 651–52 whydoenetic and, 515 pyglutamic capsule untiphagocytic anthrax and, 647–48, 651–52 disconding disconding and apathogens, 424–25 Posttranscriptional regulation homology-dependent gene silencing in fungi and, 390–95

periplasmic stress and extracytoplasmic function sigma factors, 591–617 thiol-redox pathways and, 37–39

Proteobacteria

β-subclass ammonia-oxidizing bacteria and, 485–517

Proteolytic activation anthrax and, 647

Proteomes

horizontal gene transfer in prokaryotes and, 719

Proteus spp.

bacterial gliding motility and, 50 coliform group

bacteriology and, 206 novel thiols and, 347

Providencia spp. coliform group

bacteriology and, 206

Pseudodisaccharide novel thiols and, 333

Pseudomonas aereofaciens quorum sensing and, 174

Pseudomonas aeruginosa bacterial gliding motility and, 50, 52–55, 60 fatty acid antibiotics and,

308-9, 323

history of research, 16 horizontal gene transfer in prokaryotes and, 716, 719–22, 724, 726–28

periplasmic stress and extracytoplasmic function sigma factors, 601-3

polarized epithelium and pathogens, 423–24 quorum sensing and, 167–74

Pseudomonas spp.

dairy bacteria phages and, 287 history of research, 7, 16 horizontal gene transfer in prokaryotes and, 735 novel thiols and, 347 polarized epithelium and pathogens, 412

Pseudomonas syringae periplasmic stress and extracytoplasmic function sigma factors, 596

Pseudosterilization nonreplicating latency of Mycobacterium tuberculosis and, 144

Psychrophiles history of research, 8 Psychrotrophic organisms

coliform group bacteriology and, 201, 215-17, 219-21

Public health concerns coliform group bacteriology and, 201-24

Pyrazinamide nonreplicating latency of Mycobacterium

tuberculosis and, 144 Pyrimidines history of research,

14-15
Pyrococcus spp.
horizontal gene transfer in prokaryotes and, 720, 726-27

Q

Qid3 gene hydrophobins and, 626–27

Quelling homology-dependent gene silencing in fungi and, 390-91

Quorum sensing
Agrobacterium tumefaciens
TraI/TraR virulence
system, 171–72

Bacillus subtilis

ComP/ComA competence sporulation system, 179–81

conclusions, 188–89 Erwinia carotovora

ExpI/ExpR-CarI/CarR virulence/antibiotic system, 172–73

future research, 188–89 gram-negative bacteria, 167–77

gram-positive bacteria, 177-82

hybrid homoserine lactone/two component signaling circuit, 183–85

intergenera and interkingdom

communication, 187-88

introduction, 166

Lux1/LuxR-type quorum sensing, 167–77

LuxR-like proteins, 176–77 LuxS family of AI-2

synthases, 185–86

Myxococcus xanthus,

186–87 peptide-mediated, 177–82 Pseudomonas aeruginosa

LasI/LasR-Rh1I/Rh1R virulence system, 168-71

Staphylococcus aureus AgrC/AgrA virulence system, 181–82

Streptococcus pneumoniae ComD/ComE competence system, 179

two-component interspecies

communication, 185-86 Vibrio harveyi multi-channel Lux circuit,

183-85

Vibro fischeri Lux/LuxR bioluminescence system, 167–68

and, 673-97

Redox potential

### R thiol-redox pathways and, Ribosomal RNA (rRNA) rlt phage 21-40 operon dairy bacteria phages and, Red Queen theory ammonia-oxidizing 283, 285-86 symbiosis and bacteria and, 507 fungus-growing ants, Ricinus communis Rahnella spp. coliform group 366-67 biological weapons and, bacteriology and, 206, Redundancy 236 209, 215-17, 221 thiol-redox pathways and. Rickettsia spp. Ralstonia solanacearum 28-30 biological weapons and. 236-37 quorum sensing and, Repeat-induced point horizontal gene transfer in mutations Rash homology-dependent gene prokaryotes and, 709, toxic shock syndrome and, silencing in fungi and, 716, 719-22, 728, 736 77, 80, 82 382-84 Rifampin Respiration Reactivation nonreplicating latency of periodic big bacteria and, 105, Mycobacterium immune checkpoints in 114 tuberculosis and, 144 Restriction fragment length viral latency and, 531 Rifamycin recA gene polymorphisms (RFLPs) nonreplicating latency of recombination and ammonia-oxidizing Mycobacterium bacterial population bacteria and, 509 tuberculosis and, 144 novel thiols and, 345 structure, 563 Restriction/modification Receptors bacteriophage therapy and, Rifapentene anthrax and, 647, 655 444 nonreplicating latency of antigenic variation at red Reynolds number Mycobacterium cell surface in malaria big bacteria and, 115 tuberculosis and, 144 and, 681-83 Rhizobium etli rif genes polarized epithelium and quorum sensing and, antigenic variation at red pathogens, 413-15 175 cell surface in malaria toxic shock syndrome and, and 693-94 rhl genes 77, 79, 91 quorum sensing and, 170 novel thiols and, 345 vector biology of Rhodobacter capsulatus RIM101 gene leishmaniasis and, 468-69 thiol-redox pathways and, fungal pathogenesis and, viruses and interferons. 34 754 261, 270 Rhodobacter sphaeroides Rimicaris exoculata Recombination quorum sensing and, 175 big bacteria and, 120 bacterial population thiol-redox pathways and, RNA interference (RNAi) structure and, 561-85 homology-dependent gene Recurrence Rhodococcus rhodochrous silencing in fungi and, novel thiols and, 338, 341 periodic 392-93 immune checkpoints in Ribonucleotide reductase RNA polymerase viral latency and, 531 thiol-redox pathways and, horizontal gene transfer in Red blood cells 28-29, 38 prokaryotes and, 736 antigenic variation at red 16S Ribosomal DNA (16S nonreplicating latency of cell surface in malaria rDNA) Mycobacterium

ammonia-oxidizing

bacteria and, 492-508

tuberculosis and, 144

periplasmic stress and

extracytoplasmic function sigma factors, 592, 597–98, 600

RodA gene

hydrophobins and, 626-27 Rod-shaped bacteria anthrax and, 647-63

rpo genes

bacterial gliding motility and, 53 periplasmic stress and

extracytoplasmic function sigma factors, 592, 598–99, 601–3, 611, 614 quorum sensing and, 170

rse genes

periplasmic stress and extracytoplasmic function sigma factors, 599, 601

Run-and-tumble mechanism big bacteria and, 111

S

Saccharomyces cerevisiae fungal pathogenesis and, 746-47, 751-52

horizontal gene transfer in prokaryotes and, 716, 726–28

thiol-redox pathways and, 26

Saimiri spp.

antigenic variation at red cell surface in malaria and, 677–78

Saliva

vector biology of leishmaniasis and, 473–75

Salmonella spp.

bacteriophage therapy and, 438-39

coliform group

bacteriology and, 206 polarized epithelium and pathogens, 412, 416–17 quorum sensing and, 186 recombination and bacterial population structure, 566, 569, 572, 580, 584

Salmonella typhimurium bacterial gliding motility and, 58 biological weapons and, 239

239

fatty acid antibiotics and, 308

history of research, 15 quorum sensing and, 175, 183, 186

Salmonella typhosa biological weapons

biological weapons and, 237

Sand flies

vector biology and, 453–75 sap genes anthrax and, 653, 660 fungal pathogenesis and.

SC genes

749-50

hydrophobins and, 626–31, 634, 636, 638–40

Schizont infected cell agllutination (SICA) test antigenic variation at red cell surface in malaria and, 677–78

Schizophyllum commune hydrophobins and, 626–32, 634, 636, 638–40

Schizosaccharomyces pombe fungal pathogenesis and, 756

horizontal gene transfer in prokaryotes and, 726-27

Scolytus multistriatus hydrophobins and, 636

sea gene toxic shock syndrome and,

89 seb gene

toxic shock syndrome and,

sec gene

toxic shock syndrome and,

Secondary cultures

bacteriophage therapy and, 441

sed gene

toxic shock syndrome and, 89

Sediment-water interface big bacteria and, 112-15

see gene

toxic shock syndrome and, 89

seg gene

toxic shock syndrome and,

sei gene

toxic shock syndrome and, 89

sej gene

toxic shock syndrome and, 89

sek gene

toxic shock syndrome and, 88-89

sel gene

toxic shock syndrome and, 88-89

Selection pressure

antigenic variation at red cell surface in malaria and, 678

big bacteria and, 105 horizontal gene transfer in prokaryotes and, 709

Self-assembly hydrophobins and, 625, 628–30

"Self" DNA

recombination and bacterial population structure, 581

sep gene

toxic shock syndrome and,

Sequestration

antigenic variation at red

cell surface in malaria and, 673-64 Sericomyrmex spp. symbiosis and fungus-growing ants, 359 165-89, 165 Serratia spp. bacterial gliding motility 270-71 and, 50 Single-locus variants coliform group recombination and bacteriology and, 206-8, 215-19, 221 quorum sensing and, 175, Siphoviridae 188 Sewage ammonia-oxidizing bacteria and, 497-99 skp genes sglK gene bacterial gliding motility and, 57 she gene S-laver toxic shock syndrome and, 89 Shigella spp. Social gliding motility bacteriophage therapy and, 438-39 and, 49, 54-57 biological weapons and, Sodium hypochlorite 237 244, 247-48 coliform group Sodium thiosulfate bacteriology and, 206, polarized epithelium and 244 pathogens, 419-20 "Soviet taint" sig genes 437, 441 anthrax and, 660 periplasmic stress and soxS gene extracytoplasmic function sigma factors, 602, 604-5 319 σ<sup>B</sup> factor Specialist pathogens anthrax and, 660 symbiosis and  $\sigma^{\rm E}$  envelope stress response periplasmic stress and 369-70 extracytoplasmic function sigma factors, 591-617

Signal transduction

730, 735

horizontal gene transfer in

prokaryotes and, 724-26,

periplasmic stress and thiol-redox pathways and, extracytoplasmic function 28 - 30sigma factors, 591-617 spe genes toxic shock syndrome quorum sensing and, and, 90 viruses and interferons, Spirochaetales 255-58, 261-63, 267, horizontal gene transfer in prokaryotes and, 719 Splits decomposition analysis recombination and bacterial population bacterial population structure, 576-79 structure, 566, 568 Sporothrix schenkii dairy bacteria phages and, fungal pathogenesis and, 283, 285-87, 289, 297 758 Sporulation anthrax and, 647-63 periplasmic stress and extracytoplasmic function quorum sensing and, 165, 179-82, 186-87 sigma factors, 594, 599 SrH1 gene anthrax and, 647-48, hydrophobins and, 651-54, 659-60 626-27 ssa gene toxic shock syndrome and, bacterial gliding motility 90 SsgA gene biological weapons and, hydrophobins and, 626-27, Stachybotrys spp. biological weapons and, biological weapons and, fungal pathogenesis and, 755 bacteriophage therapy and, Staphylococcus aureus biological weapons and, fatty acid antibiotics and, fatty acid antibiotics and, 308, 319 quorum sensing and, 179, fungus-growing ants, 181-82, 186 recombination and Specific parasitic cell forms bacterial population structure, 561, 575, 578, fungal pathogenesis and, 751-52 581-82 Specificity toxic shock syndrome and,

77-94

Staphylococcus spp.

bacteriophage therapy and,

443

bacteriophage therapy and, 440, 442 novel thiols and, 347 Staphylothermus marinus big bacteria and, 115, 117 Star evolution horizontal gene transfer in prokaryotes and, 714 STAT proteins viruses and interferons. 255-58, 261-63, 270-74 Stationary state nonreplicating latency of Mycobacterium tuberculosis and, 139-56 STE12 gene fungal pathogenesis and, 752, 756 stevor gene antigenic variation at red cell surface in malaria and, 693-94

Stigmatella aurantiaca bacterial gliding motility and, 58

Streptococcus pneumoniae fatty acid antibiotics and, 308-9, 319, 324 polarized epithelium and pathogens, 413-14

quorum sensing and, 179-80, 186

recombination and bacterial population structure, 561, 575, 578, 580-82, 584

Streptococcus pyogenes quorum sensing and, 186 recombination and

bacterial population structure, 575, 581 toxic shock syndrome and, 77-94

Streptococcus spp. coliform group bacteriology and, 212 dairy bacteria phages and, 283, 287-89, 291-95 horizontal gene transfer in prokaryotes and, 735 novel thiols and, 347-48

Streptomyces spp.

fatty acid antibiotics and, 306, 314 hydrophobins and, 631 novel thiols and, 343,

periplasmic stress and extracytoplasmic function sigma factors, 596-97, 602, 605

quorum sensing and, 166 thiol-redox pathways and,

Substrate monopolization big bacteria and, 128,

Sulfide-oxidizing bacteria big bacteria and, 105-32

Sulfidic mud big bacteria and, 105 Sulfolobus acidocauldarius novel thiols and, 338

Sulfur bacteria big bacteria and, 105-32

Superantigens bacterial toxic shock syndrome and, 77-94

supp gene thiol-redox pathways and, 38-39

surA gene periplasmic stress and extracytoplasmic function sigma factors, 594

Surface antigen proteins variant

antigenic variation at red cell surface in malaria and, 677-78

Switching antigenic variation at red

cell surface in malaria and, 678-79, 692-93. 696-97 fungal pathogenesis and, 753-54

**Symbiosis** 

fungus-growing ants and ant genera, 358-60 antibiotic production by Attine ants, 364-66 antibiotic-producing bacteria, 371-74 antibiotics produced by fungal cultivars, 365 Attine fungus gardens, 368-69 benefite to actinomycete, 374 coevolution, 361-62 conclusions, 375 Escovopsis spp., 368-69 fungal cultivation. 360-61 future research, 374-75 garden-tending, 362-66 introduction, 358 manuring and promoting garden growth, 363 monocultures, 366-67 pathogens of ant gardens, 367-71 promoting competitive ability of cultivar, 364 protecting garden from alien microbes, 363-66 Red Queen theory, 366-67 specialist vs generalist garden pathogens.

369-70 taxonomy, 370-71 horizontal gene transfer in prokaryotes and, 709 quorum sensing and, 165 Synechocystis spp. bacterial gliding motility

and, 49, 60, 68

ammonia-oxidizing

Thiols

definition, 79-80

horizontal gene transfer in bacteria and, 494 novel prokaryotes and, 711, Thermodiscus spp. conclusions, 348-49 716, 720-21, 724, big bacteria and, 117 ergothioneine, 346-48 glutathione derivatives, 726-28 Thermoplasma acidophilum 2-5(A)-Synthetase/Rnase L horizontal gene transfer in 336-37 viruses and interferons. prokaryotes and, 720-21 introduction, 334 miscellaneous thiols, 264-65 Thermotoga maritima Systemic fungal infections horizontal gene transfer in 348 fungal pathogenesis and, prokaryotes and, 711, mycothiol, 343-46 743, 761-63 716, 720-21, 723, 726-28 novel vs common thiols. Thermotrophic organisms 335 T coliform group oxidation, 334-35 Tail proteins bacteriology and, 201, Thiomargarita namibiensis dairy bacteria phages and, 219-21 big bacteria and, 105-6, 294-95 108, 115-17, 129-31 Thermus thermophilus Tatumella spp. horizontal gene transfer in Thioplica spp. coliform group prokaryotes and, 726-27 big bacteria and, 116-17, bacteriology and, 206 125, 128-31 **Thigmotropism** fungal pathogenesis and, Thioredoxin/thioredoxin Taxonomy 748 coliform group reductase bacteriology and, 201-24 Thiol-redox pathways thiol-redox pathways and, symbiosis and conclusions, 39-40 21, 23-26 fungus-growing ants, cytoplasm, 23-30, 37-39 Thiothrix spp. 370-71 DsbA, 31-32 big bacteria and, 120-21, T-cell memory DsbB, 32-33 125, 131 immune checkpoints in DsbC, 31-32 Thiovulum majus viral latency and, 531, DsbD, 34-36 big bacteria and, 105, 533-53 glutaredoxin/glutathione/ 111-13, 117, 123-24 T-cell stimulation glutathione reductase. Thogoto virus toxic shock syndrome and. 26 - 28viruses and interferons, 268 77, 79, 85, 91, 93 introduction, 22-23 Tight junctions Terminal restriction fragment miscellaneous periplasmic polarized epithelium and length polymorphism thiol-redox proteins. pathogens, 424-25 (T-RFLP) analysis 36-37 Titanospirillum velox oxidation, 32-33 ammonia-oxidizing big bacteria and, 117 bacteria and, 511, 516 oxidative protein folding, Toxic shock syndrome Terrestrial environments 37-39 animal models, 93-94 ammonia-oxidizing periplasm, 30-37 bacterial superantigens bacteria and, 499-502 reduction, 34-36 MHC class II. 91-93 Tetracyclines redundancy vs specificity, structure and function. bacteriophage therapy and, 28 - 3090-94 440, 446-47 thioredoxin/thioredoxin T cell anergy and tgl gene reductase, 23-26 deletion, 93 bacterial gliding motility Thiolactomycin T-cell antigen receptor, and, 55-56 fatty acid antibiotics and, 305-6, 314-16 Thermodesulfovibrio spp. clinical features, 79-86

**UPGMA** algorithm

recombination and

bacterial population

epidemiology, 79-86 Transcriptional regulation Tri genes future research, 94 dairy bacteria phages and, hydrophobins and, 626-27 host immunity, 85-86 289-90 Trimethoprim/sulfafurazole introduction, 78-79 thiol-redox pathways and, bacteriophage therapy and, 447 phylogenetic tree, 88 staphylococcal viruses and interferons, Tritrichomonas foetus epidemiology, 81-82 255-61, 267 novel thiols and, 335 genetics, 87-89 Transcytosis trp gene overview, 80-81 polarized epithelium and toxic shock syndrome and. streptococcal pathogens, 413-14 88 epidemiology, 83-84 Transient clones trx genes genetics, 90 recombination and thiol-redox pathways and, overview, 82-83 bacterial population 24-30, 37-39 superantigen structure, 573 Trypanosoma brucei "superfamily", 86-87 Translocation antigenic variation at red treatment, 84-85 thiol-redox pathways and, cell surface in malaria Toxins and, 678, 673 anthrax and, 647 Transnuclear transcriptional fungal pathogenesis and, fungal pathogenesis and, gene silencing 756 754-55 homology-dependent gene TSST-huvine hydrophobins and, 625, silencing in fungi and, toxic shock syndrome and, 386-87 86 toxic shock syndrome and, trb operon tst genes 77-94 quorum sensing and, toxic shock syndrome and, 86-89 Toxoids 172 toxic shock syndrome and, Treponema pallidum Twitching motility 86 antigenic variation at red bacterial gliding motility Toxoplasma gondii cell surface in malaria and, 49, 52-54 fatty acid antibiotics and, and, 676 Type IV pilus 316 horizontal gene transfer in bacterial gliding motility and, 49-69 viruses and interferons, prokaryotes and, 716, 273 719-23, 726-27 tvrB gene Trichoderma spp. toxic shock syndrome and, Trabulsiella spp. biological weapons and, 88 coliform group bacteriology and, 206, 626-27, 629 U 209 hydrophobins and, 626-27, 629 Trachymyrmex spp. ubiA gene thiol-redox pathways and, symbiosis and symbiosis and fungus-growing ants, 359, fungus-growing ants, 369 32 370, 372 Trichomonas vaginalis Ultramicrobacteria TraI/TraR virulence system novel thiols and, 335 big bacteria and, 106 "Unicity" quorum sensing and, Trichosporon spp. 171 - 72fungal pathogenesis and, bacteriophage therapy and, 762 442 Transcriptional gene silencing

homology-dependent gene

silencing in fungi and,

382-90

Triclosan

fatty acid antibiotics and,

305-6, 318-19

quorum sensing and, 175

bacteriophage therapy and,

Vibrio cholerae

446

structure, 576, 580-81 biological weapons and, interferons and, 255-75 237 Virus-host regulatory loop Upregulation periplasmic stress and fatty acid antibiotics and. immune checkpoints in viral latency and, 531 322-23 extracytoplasmic function sigma factors, 595-96 horizontal gene transfer in VMH genes Ureaplasma urealyticum prokaryotes and, 716, hydrophobins and, 626-27 719-20, 722-23, horizontal gene transfer in Vorticella spp. prokaryotes and, 716, 726-27 big bacteria and, 719-20 quorum sensing and, 186 115 Ustilago maydis Vibrio spp. W hydrophobins and, 626-27 bacterial gliding motility and, 50 Wangiella dermatitidis novel thiols and, 347 fungal pathogenesis and, Vaccines quorum sensing and, 755 anthrax and, 647, 651, 166-68, 172-74, 183-86, Water safety 188 microbial antigenic variation at red Viral latency coliform group cell surface in malaria immune checkpoints and, bacteriology and, and, 680 531-53 201 - 24bacteriophage therapy and. Virulence 440, 442-43, 445 anthrax and, 647, 650-51. X toxic shock syndrome and, 658-59 Xantheria ectaneoides antigenic variation at red hydrophobins and, 626-27 86 cell surface in malaria Xanthobacter spp. var genes antigenic variation at red and, 673, 681-87, 697 novel thiols and, 338, 341 cell surface in malaria dairy bacteria phages and, Xanthoria spp. and, 673, 686-93 283, 287 hydrophobins and, 626-27, Variable-number tandem fungal pathogenesis and, 635 repeats (VNTRs) 743-63 XEH1 gene anthrax and, 663 periplasmic stress and hydrophobins and, 626-27 Xenologous gene Vector-host interactions extracytoplasmic function leishmaniasis and, 453-75 sigma factors, 615-16 displacement Vertical descent polarized epithelium and horizontal gene transfer in horizontal gene transfer in pathogens, 407 prokaryotes and, 709, prokaryotes and, 711-12 quorum sensing and, 165. 718, 727, 734-36 Vertical transmission 168-73, 181-82 Xenorhabdus spp. symbiosis and symbiosis and coliform group fungus-growing ants, fungus-growing ants, 357, bacteriology and, 206 361 368-75 XPH1 gene Vesicular stomatitis virus Viruses hydrophobins and, viruses and interferons. bacteriophage therapy and. 626-27 268-69 Xylella fastidiosa Vibrio anguillarum biological weapons and, horizontal gene transfer in

236, 240, 244, 247

viral latency and,

531-53

immune checkpoints in

prokaryotes and, 716,

hydrophobins and, 637

720, 722, 724-27

Xylem

Y

Yersinia pestis biological weapons and, 236-37, 239, 247

Yersinia spp. coliform group bacteriology and, 206-8, 214-16, 219,

221

polarized epithelium and pathogens, 421-23 quorum sensing and, 175, 186

recombination and bacterial population structure, 564, 584

Yokenella spp.

coliform group

bacteriology and, 206, 209

7

Zn2+ metalloprotease anthrax and, 647, 657 Zoothamnium spp. big bacteria and, 115